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## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: The Wistar Institute  
Bayer Corporation
- (ii) TITLE OF INVENTION: Peptides and Peptidomimetics with  
Structural Similarity to Human p53 That Activate p53  
Function
- (iii) NUMBER OF SEQUENCES: 35
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Banner & Allegretti, Ltd.
  - (B) STREET: 1001 G Street, N.W.
  - (C) CITY: Washington, D.C.
  - (D) STATE: District of Columbia
  - (E) COUNTRY: U.S.
  - (F) ZIP: 20001
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA: PCT
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA: USA
  - (A) APPLICATION NUMBER: 08/392,542
  - (B) FILING DATE: 02-16-95
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Hoscheit, Dale H.
  - (B) REGISTRATION NUMBER: 19,090
  - (C) REFERENCE/DOCKET NUMBER: 0486.53880
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 202 508-9100
  - (B) TELEFAX: 202 508-9299

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1317 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCTAGAGCC ACCGTCCAGG GAGCAGGTAG CTGCTGGGCT CCGGGGACAC TTTGCGTTCCG

GGCTGGGAGC GTGCTTTCCA CGACGGTGAC ACGCTTCCCT GGATTGGCAG CCAGACTGCC 120  
 TTCCGGGTCA CTGCCATGGA GGAGCCGCAG TCAGATCCTA GCGTCGAGCC CCCTCTGAGT 180  
 CAGGAAACAT TTTCAGACCT ATGGAAACTA CTTCTGAAA ACAACGTTCT GTCCCCCTTG 240  
 CCGTCCCAAG CAATGGATGA TTTGATGCTG TCCCCGGACG ATATTGAACA ATGGTTCACT 300  
 GAAGACCCAG GTCCAGATGA AGCTCCAGA ATGCCAGAGG CTGCTCCCCC CGTGGCCCCCT 360  
 GCACCAGCAG CTCCTACACC GGCGGCCCCCT GCACCAGCCC CCTCCTGGCC CCTGTCATCT 420  
 TCTGTCCCTT CCCAGAAAAC CTACCAGGGC AGCTACGGTT TCCGTCTGGG CTTCTTGCACT 480  
 TCTGGGACAG CCAAGTCTGT GACTTGCACG TACTCCCCTG CCCTCAACAA GATGTTTTGC 540  
 CAACTGGCCA AGACCTGCCC TGTGCAGCTG TGGGTTGATT CCACACCCCC GCCCGGCACC 600  
 CGCGTCCGCG CCATGGCCAT CTACAAGCAG TCACAGCACA TGACGGAGGT TGTGAGGCGC 660  
 TGCCCCCACC ATGAGCGCTG CTCAGATAGC GATGGTCTGG CCCCTCCTCA GCATCTTATC 720  
 CGAGTGGAAG GAAATTTGCG TGTGGAGTAT TTGGATGACA GAAACACTTT TCGACATAGT 780  
 GTGGTGGTGC CCTATGAGCC GCCTGAGGTT GGCTCTGACT GTACCACCAT CCACTACAAC 840  
 TACATGTGTA ACAGTTCCTG CATGGGCGGC ATGAACCGGA GGCCCATCCT CACCATCATC 900  
 ACACTGGAAG ACTCCAGTGG TAATCTACTG GGACGGAACA GCTTTGAGGT GCGTGTGTTGT 960  
 GCCTGTCTCTG GGAGAGACCG GCGCACAGAG GAAGAGAATC TCCGCAAGAA AGGGGAGCCT 1020  
 CACCACGAGC TGCCCCCAGG GAGCACTAAG CGAGCACTGC CCAACAACAC CAGCTCCTCT 1080  
 CCCCAGCCAA AGAAGAAACC ACTGGATGGA GAATATTTCA CCCTTCAGAT CCGTGGGCGT 1140  
 GAGCGCTTCG AGATGTTCCG AGAGCTGAAT GAGGCCTTGG AACTCAAGGA TGCCCAGGCT 1200  
 GGAAGGAGC CAGGGGGGAG CAGGGCTCAC TCCAGCCACC TGAAGTCCAA AAAGGGTCAG 1260  
 TCTACCTCCC GCCATAAAAA ACTCATGTTT AAGACAGAAG GGCCTGACTC AGACTGA 1317

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 393 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	Glu	Pro	Gln	Ser	Asp	Pro	Ser	Val	Glu	Pro	Pro	Leu	Ser	Gln
1				5					10					15	
Glu	Thr	Phe	Ser	Asp	Leu	Trp	Lys	Leu	Leu	Pro	Glu	Asn	Asn	Val	Leu
			20					25					30		

[illegible]

Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu Met  
 370 375 380

Phe Lys Thr Glu Gly Pro Asp Ser Asp  
 385 390

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 390 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Mus spretus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Thr Ala Met Glu Ser Gln Ser Asp Ile Ser Leu Glu Leu Pro  
 1 5 10 15  
 Leu Ser Gln Glu Thr Phe Ser Gly Leu Trp Lys Leu Leu Pro Pro Glu  
 20 25 30  
 Asp Ile Leu Pro Ser Pro His Cys Met Asp Asp Leu Leu Leu Pro Gln  
 35 40 45  
 Asp Val Glu Glu Phe Phe Glu Gly Pro Ser Glu Ala Leu Arg Val Ser  
 50 55 60  
 Gly Ala Pro Ala Ala Gln Asp Pro Val Thr Glu Thr Pro Gly Pro Val  
 65 70 75 80  
 Ala Pro Ala Pro Ala Thr Pro Trp Pro Leu Ser Ser Phe Val Pro Ser  
 85 90 95  
 Gln Lys Thr Tyr Gln Gly Asn Tyr Gly Phe His Leu Gly Phe Leu Gln  
 100 105 110  
 Ser Gly Thr Ala Lys Ser Val Met Cys Thr Tyr Ser Pro Pro Leu Asn  
 115 120 125  
 Lys Leu Phe Cys Gln Leu Val Lys Thr Cys Pro Val Gln Leu Trp Val  
 130 135 140  
 Ser Ala Thr Pro Pro Ala Gly Ser Arg Val Arg Ala Met Ala Ile Tyr  
 145 150 155 160  
 Lys Lys Ser Gln His Met Thr Glu Val Val Arg Arg Cys Pro His His  
 165 170 175  
 Glu Arg Cys Ser Asp Gly Asp Gly Leu Ala Pro Pro Gln His Leu Ile  
 180 185 190  
 Arg Val Glu Gly Asn Leu Tyr Pro Glu Tyr Leu Glu Asp Arg Gln Thr  
 195 200 205  
 Phe Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu Ala Gly Ser  
 210 215 220

Publ. No. WO 96/25434

(2) INFORMATION FOR SEQ ID NO:4:

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

(2) INFORMATION FOR SEQ ID NO:5:

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

His Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser Arg His  
1 5 10

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Arg Ala His Ser Ser His Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser  
1 5 10 15

Arg His Lys Lys  
20

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ser His Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys  
 1 5 10 15  
 Leu Met Phe Lys  
 20

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Arg Ala His Ser Ser His Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser  
 1 5 10 15  
 Arg His Lys Lys Leu Met Phe Lys  
 20

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ser Arg Ala His Ser Ser His Leu Lys Ser Lys Lys Gly Gln Ser Thr  
 1 5 10 15  
 Ser Arg His Lys Lys Leu Met Phe Lys  
 20 25

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 27 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly Gly Ser Arg Ala His Ser Ser His Leu Lys Ser Lys Lys Gly Gln  
 1 5 10 15  
 Ser Thr Ser Arg His Lys Lys Leu Met Phe Lys  
 20 25



## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Lys Lys Ser Lys Leu His Ser Ser His Ala Arg  
1 5 10

## (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Arg Ala His Ser Ser His Leu Lys  
1 5

## (2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

His Leu Lys Ser Lys Lys  
1 5

## (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

His Leu Lys Ser Lys  
1 5

## (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu Lys Ser Lys Lys  
1 5

## (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Lys Ser Lys Lys Gly Gln  
1 5

## (2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Lys Ser Lys Lys Gly  
1 5

## (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Arg Ala His Ser His Leu Lys  
1 5

## (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

His Lys Ser Lys Lys  
1 5

## (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Cys Gly Gly Ser Arg Ala His Ser Ser His Leu Lys Ser Lys Lys Gly  
1 5 10 15

Gln Ser Thr Ser Arg His Lys Lys Leu Met Phe Lys  
20 25

## (2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Cys Gly Ser Arg Ala His Ser Ser His Leu Lys Ser Lys Lys Gly Gln  
1 5 10 15

Ser Thr Ser Arg His Lys Lys Leu Met Phe Lys  
20 25

## (2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Cys Gly Gly Ser Arg Ala His Ser Ser His Leu Lys Ser Lys Lys Gly  
 1 5 10 15  
 Gln Ser Thr Ser Arg His Lys Lys Leu Met Lys  
 20 25

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Cys Gly Ser Arg Ala His Ser Ser His Leu Lys Ser Lys Lys Gly Gln  
 1 5 10 15  
 Ser Thr Ser Arg His Lys Lys Leu Met Lys  
 20 25

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1215 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAATTCAACC AGCAGCCTCC CGCGACCATG GAGGAGCCGC AGTCAGATCC TAGCGTCGAG	60
CCCCCTCTGA GTCAGGAAAC ATTTTCAGAC CTATGGAAAC TACTTCCTGA AAACAACGTT	120
CTGTCCCCCT TGCCGTCCCA AGCAATGGAT GATTGTATGC TGTCCCCGGA CGATATTGAA	180
CAATGGTTCA CTGAAGACCC AGGTCCAGAT GAAGCTCCCA GAATGCCAGA GGCTGCTCCC	240
CCCGTGCGCC CTGCACCAGC AGCTCCTACA CCGGCCGCCC CTGCACCAGC CCCCTCCTGG	300
CCCCTGTCAT CTTCTGTCCC TTCCAGAAA ACCTACCAGG GCAGCTACGG TTTCCGTCTG	360
GGCTTCTTGC ATTCTGGGAC AGCCAAGTCT GTGACTTGCA CGTACTCCCC TGCCCTCAAC	420
AAGATGTTTT GCCAACTGGC GAAGACCTGC CCTGTGCAGC TGTGGGTTGA TTCCACACCC	480
CCGCCCCGCA CCCGCGTCCG CGCCATGGCC ATCTACAAGC AGTCACAGCA CATGACGGAG	540
GTTGTGAGGC GCTGCCCCCA CCATGAGCGC TGCTCAGATA GCGATGGTCT GGCCCCCTCCT	600
CAGCATCTTA TCCGAGTGGA AGGAAATTTG CGTGTGGAGT ATTTGGATGA CAGAAACACT	660

TTTCGACATA GTGTGGTGGT ACCCTATGAG CCGCCTGAGG TTGGCTCTGA CTGTACCACC 720  
 ATCCAATACA ACTACATGTG TAACAGTTCC TGCATGGGCG GCATGAACCG GAGGCCCCATC 780  
 CTCACCATCA TCACACTGGA AGACTCCAGT GGTAATCTAC TGGGACGGAA CAGCTTTGAG 840  
 GTGCGTGTTC GTGCCTGTCC TGGGAGAGAC CGGCGCACAG AGGAAGAGAA TCTCCGCAAG 900  
 AAAGGGGAGC CTCACCACGA GCTCCCCCCA GGGAGCACTA AGCGAGCACT GCCCAACAAC 960  
 ACCAGCTCCT CTCCCAGCC AAAGAAGAAA CCACTGGATG GAGAATATTT CACCCTTCAG 1020  
 ATCCGCGGGC GTGAGCGCTT CGAAATGTTC CGAGAGCTGA ATGAGGCCTT GGAACTCAAG 1080  
 GATGCCCAGG CTGGGAAGGA GCCAGGGGGG AGCAGGGCTC ACTCCAGCCA CCTGAAGTCC 1140  
 AAAAAGGGTC AGTCTACCTC CCGCCATAAA AAATCATGT TCAAGACAGA AGGGCCTGAC 1200  
 TCAGACTGAG TCGAC 1215

## (2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GAGAGCCCCA GTTACCATAA CTACTCT

27

## (2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATCACGTGAT ATCACGTGAT ATCACGTGAT

30

## (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCCGAACATG TCCCAACATG TTGGGG

26

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TCGAGCATGT TCGAGCATGT TCGAGCATGT

30

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCGGGCATGT CCGGGCATGT CCGGGCATGT

30

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Lys Ser Lys Lys Gln  
1 5

## (2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Arg Ala His Ser Ser His Lys Lys  
1 5

## (2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

His Leu Lys Ser Arg His  
1 5

## (2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TGGCATGTCA TGGCATGTCA